Enzyme rhythms in model ox_red_2

Model name: ox_red_2

o Optimisation problem
- Protein turnover time 1.8e+03 s = 30 min
- Perturbed parameter(s) : S
- Perturbation frequency f : 1/s (period 1 s)
- Scored quantity: red
- Scored quantity: ox
- Scored quantity: prod
- Fitness-averaged fitness
- Posttranslational rhythms allowed
- Standard frequency considered f : 1/s (period 1 s)

o Model properties:
- inactive_enzymes: 0
- balanced_reference_state: 1
- consider_external_rhythm: 1
- adaptive_rhythm: 1
- spontaneous_rhythm: 0
- spontaneous_rhythm_at_omega: 0
- has_spontaneous_rhythm_and_inactive_enzymes: 0

o No beneficial self-induced oscillation found

o Fitness changes after external perturbation at frequency f=1/s
- Change by perturbation alone (xx): -0.0106
- Change by adaption synergies (xu): 0.00594
- Change by periodic enzyme (uu): -0.0109
- Change by enzyme mean shift (u): -1.79e-08
- Total fitness change : -0.0155
- Fitness gain by adaption : -0.00494
- Maximum adaptive fitness found (in tested range) at frequency f =0.178/s (period 5.62 s)
- Predicted max. fitness change (adaptive, num. opt, full ampl. constraints) at frequency f =0.178: -0.0132

o Self-induced oscillations?
- No beneficial self-induced oscillations (2nd order, amplitude below 1/2 of mean) found at frequency f = 1/s (principal synergy = -0.531): Predicted fitness change -0.0422

o Numerical calculation (responsive, f=1)
- Fitness change (fitness-averaged): -0.0106
- Fitness change (state-averaged): -8.96e-05
o Numerical calculation (adaptive, f=1)
- Fitness change (fitness-averaged): -0.0076
- Fitness change (state-averaged): 0.0129

o Numerical calculation (self-induced rhythm, amplitude below 1/2 of mean, f=1)
- Fitness change (fitness-averaged) : 9.99e-06
- Fitness change (state-averaged): 9.99e-06

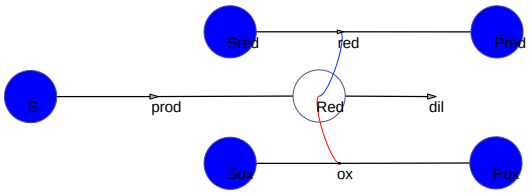


Figure 1: Network and reference flux

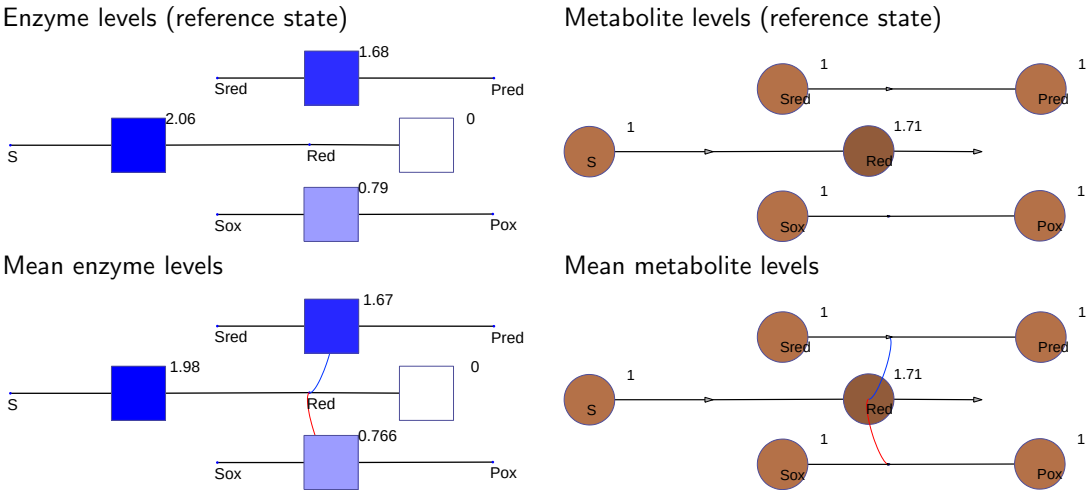


Figure 2: Reference state (top) and mean state during oscillation (bottom).

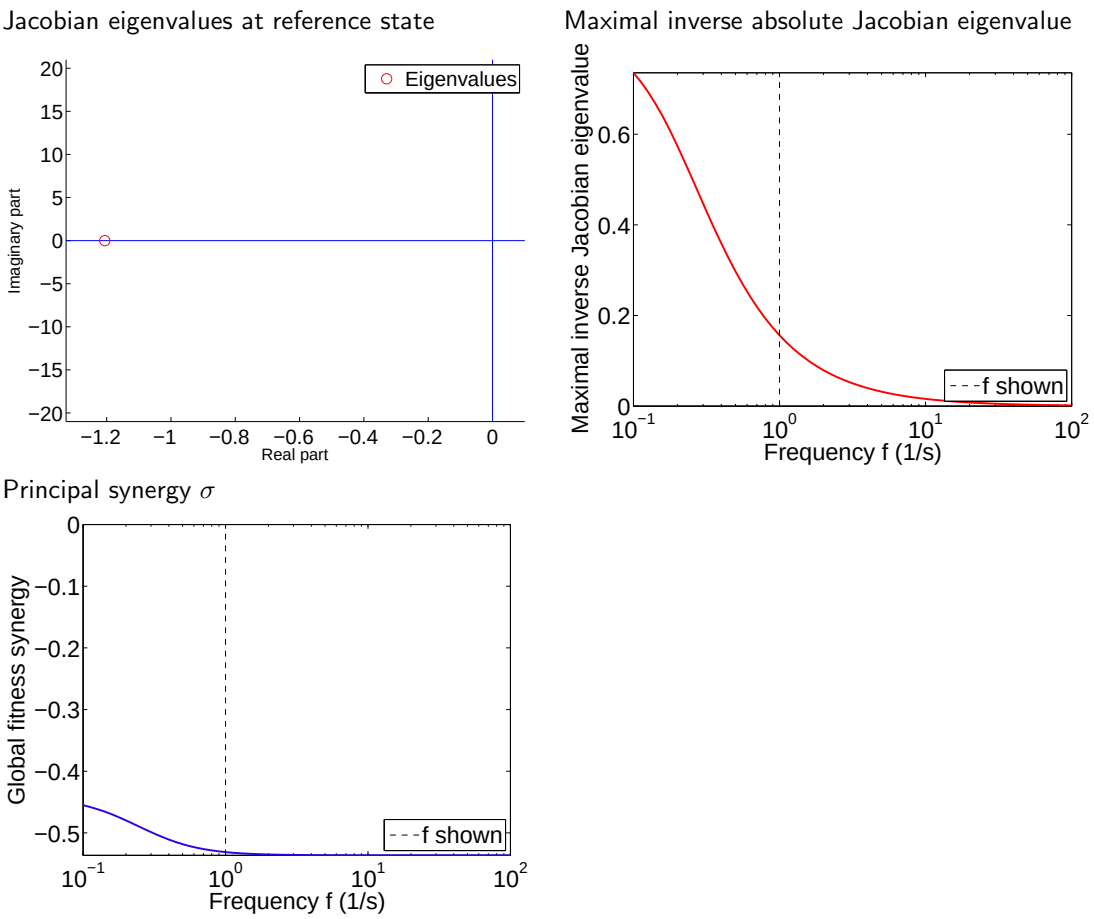
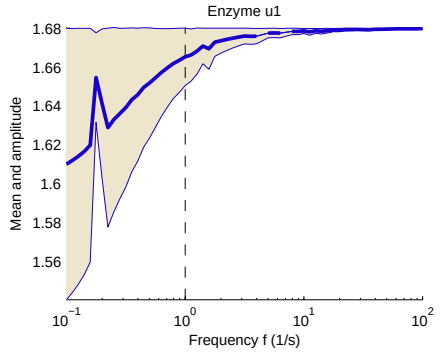
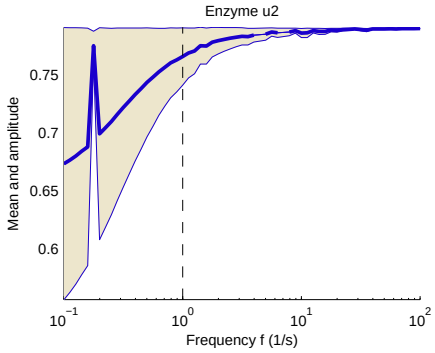
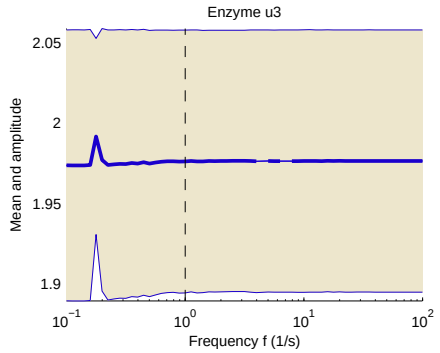


Figure 3: Control analysis. Left: Global fitness synergy (maximal fitness curvature eigenvalue), as a function of the frequency. Right: Relative amplitudes of individual enzymes for the least wasteful enzyme mode (components of the leading fitness curvature eigenvector).

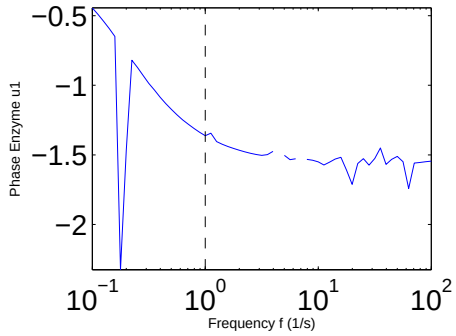
Protein level and enzyme activity (mean and amplitude)

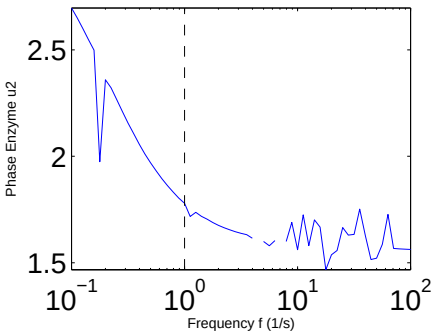


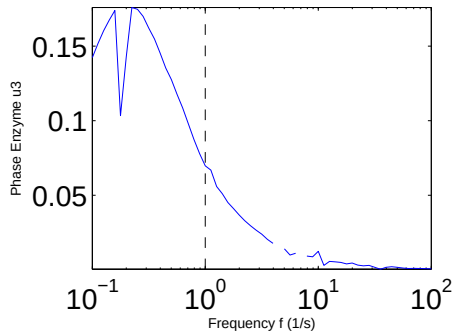




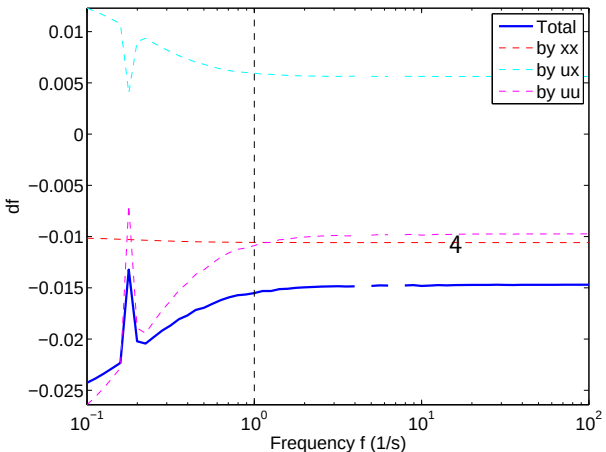
Phase angles $[0, 2\,\pi]$







Fitness change



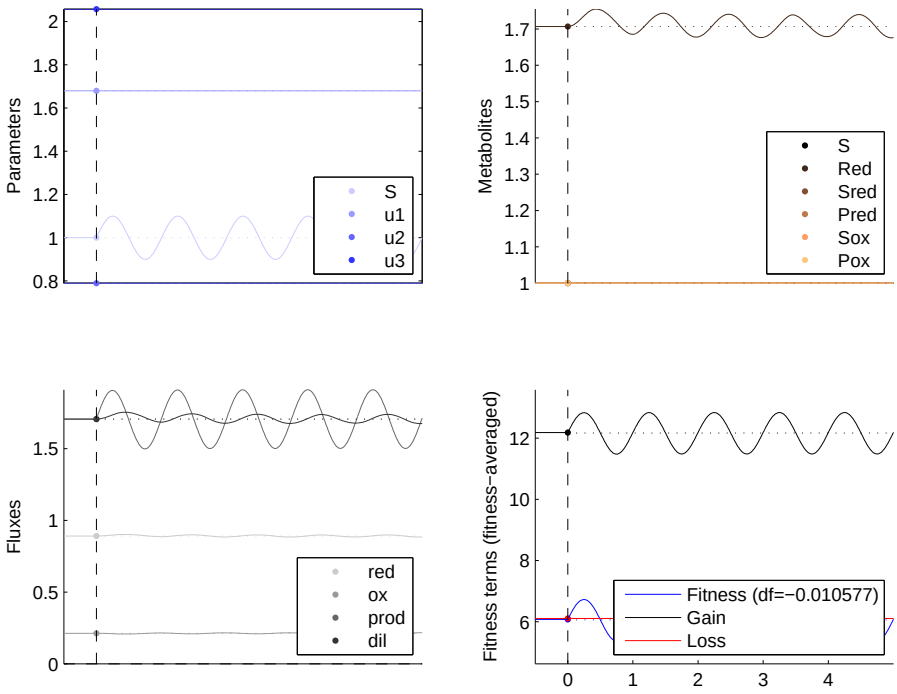


Figure 5: Numerical calculations: responsive oscillations (curves). Dynamic effects of oscillations. The panels show different types of variables: (i) Optimal periodic enzyme levels; (ii) internal metabolite levels; (iii) reaction fluxes; (iv) fitness, benefit, and cost. Perturbation frequency see first page.

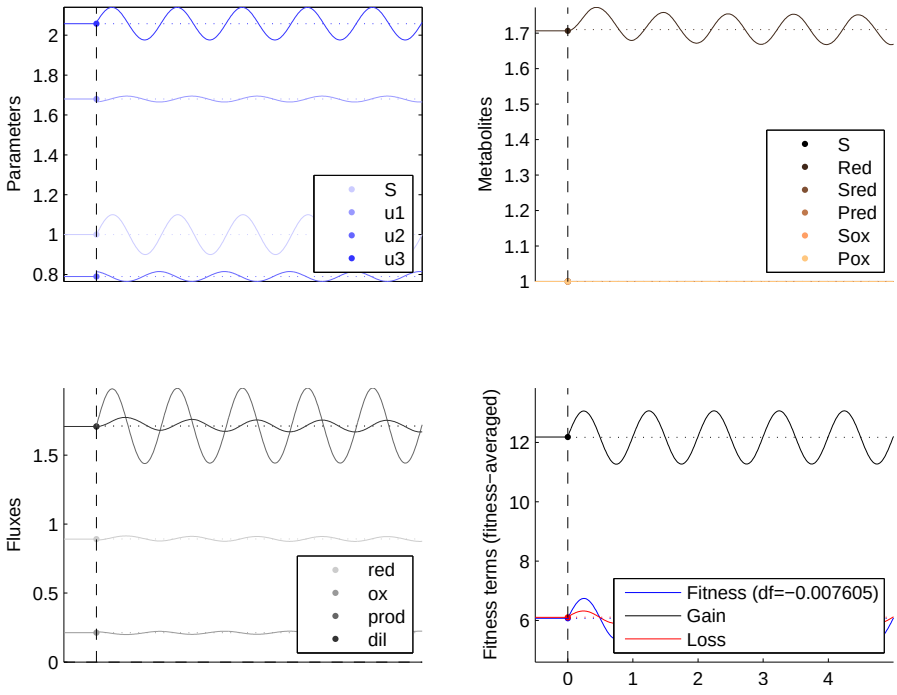


Figure 6: Numerical calculations: adaptive oscillations (curves). Dynamic effects of oscillations. The panels show different types of variables: (i) Optimal periodic enzyme levels; (ii) internal metabolite levels; (iii) reaction fluxes; (iv) fitness, benefit, and cost. Perturbation frequency see first page.

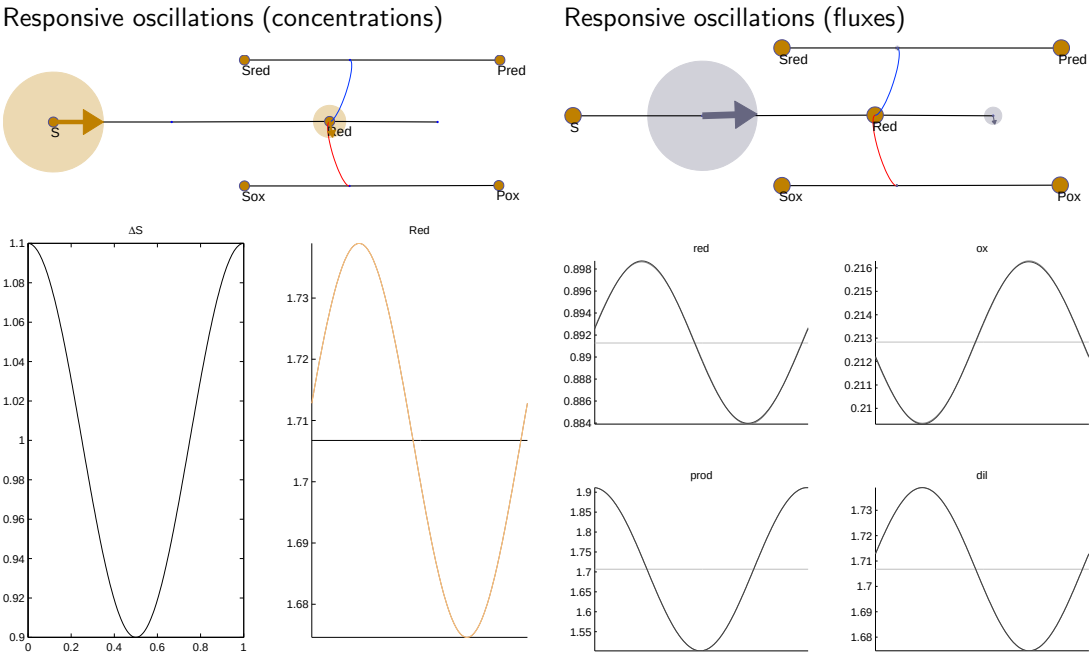


Figure 7: Responsive oscillations (local expansion; arrows: absolute changes) Perturbation frequency see first page.

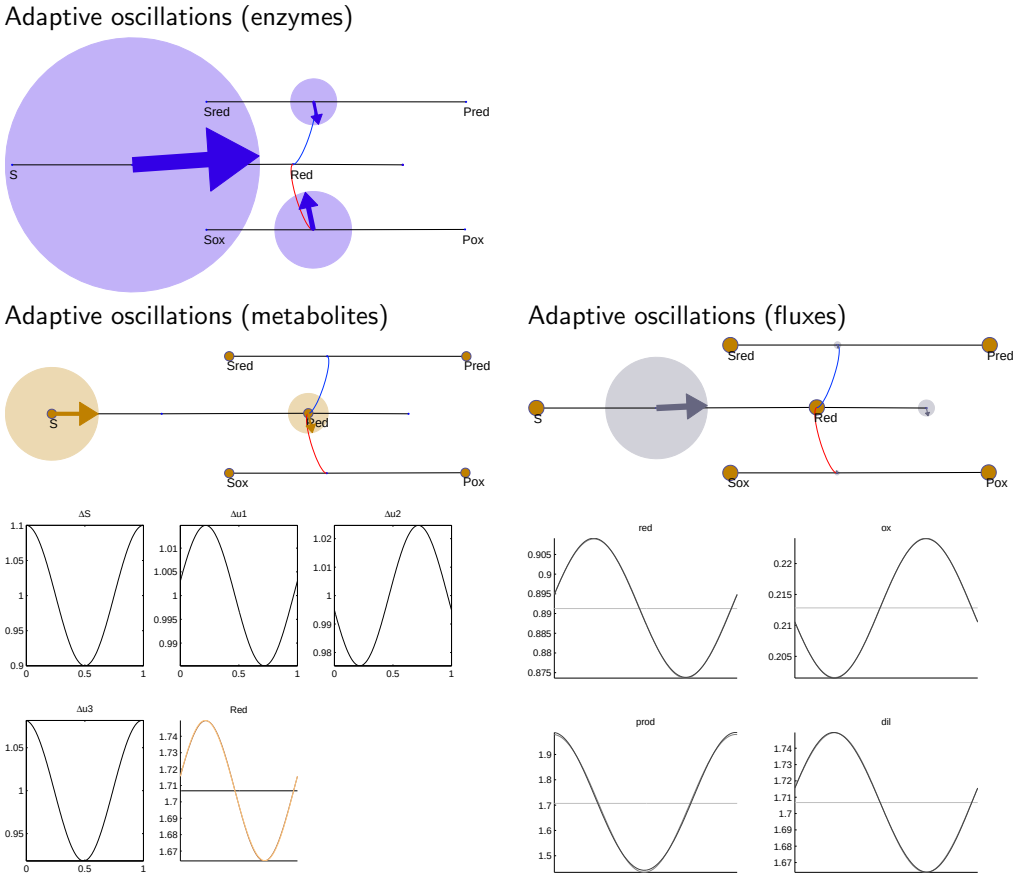


Figure 8: Adaption to forced oscillations (local expansion; arrows: absolute changes). Perturbation frequency see first page.

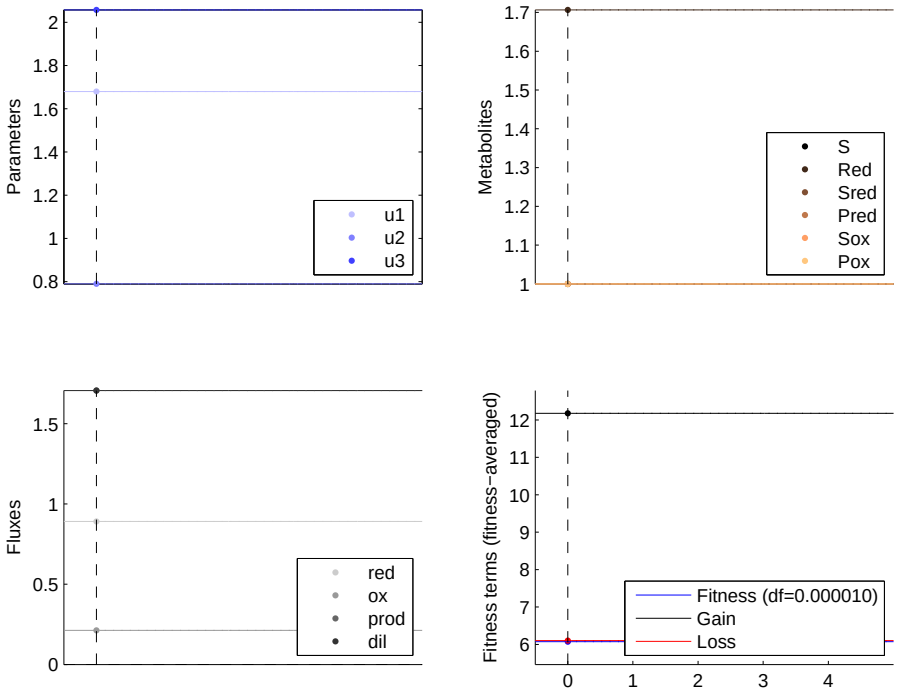


Figure 9: Tentative spontaneous oscillations. Perturbation frequency see first page.

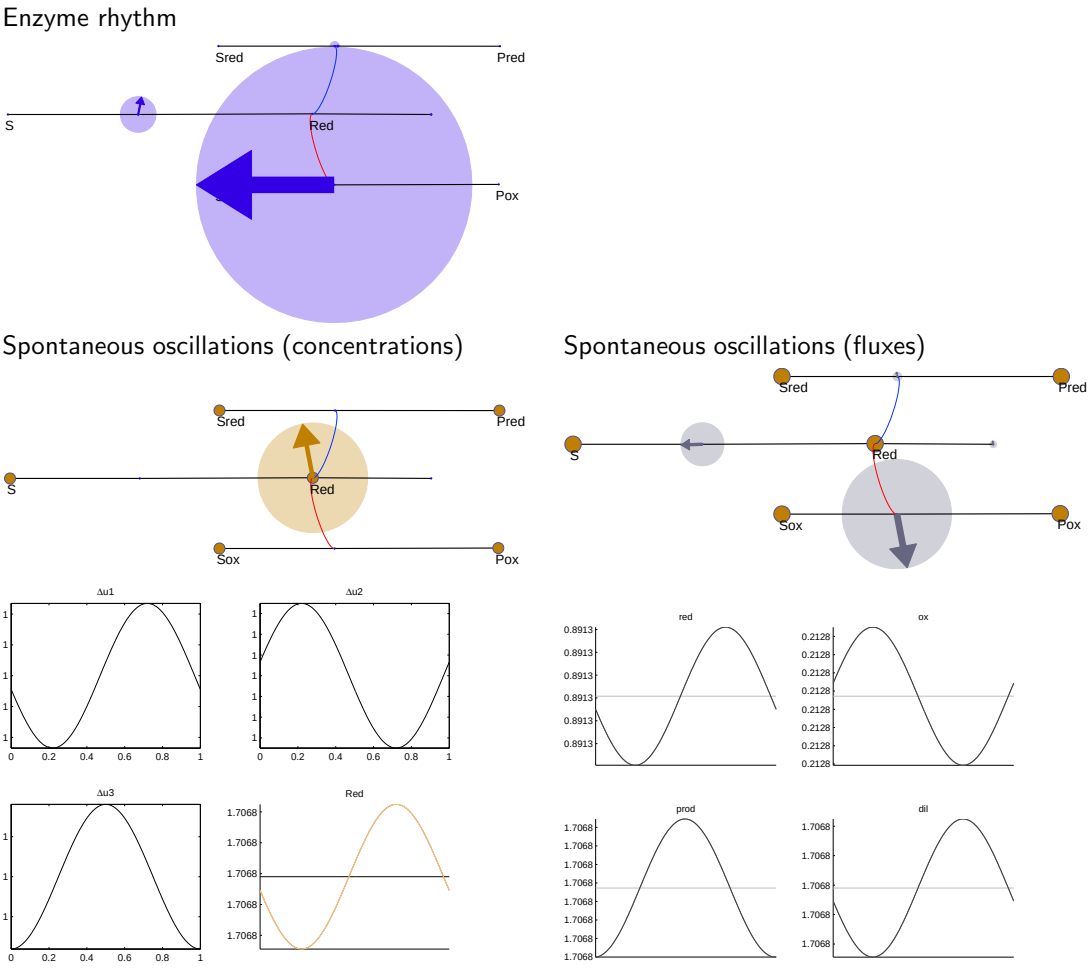


Figure 10: Tentative spontaneous oscillations (local expansion; arrows: absolute changes). Perturbation frequency see first page.

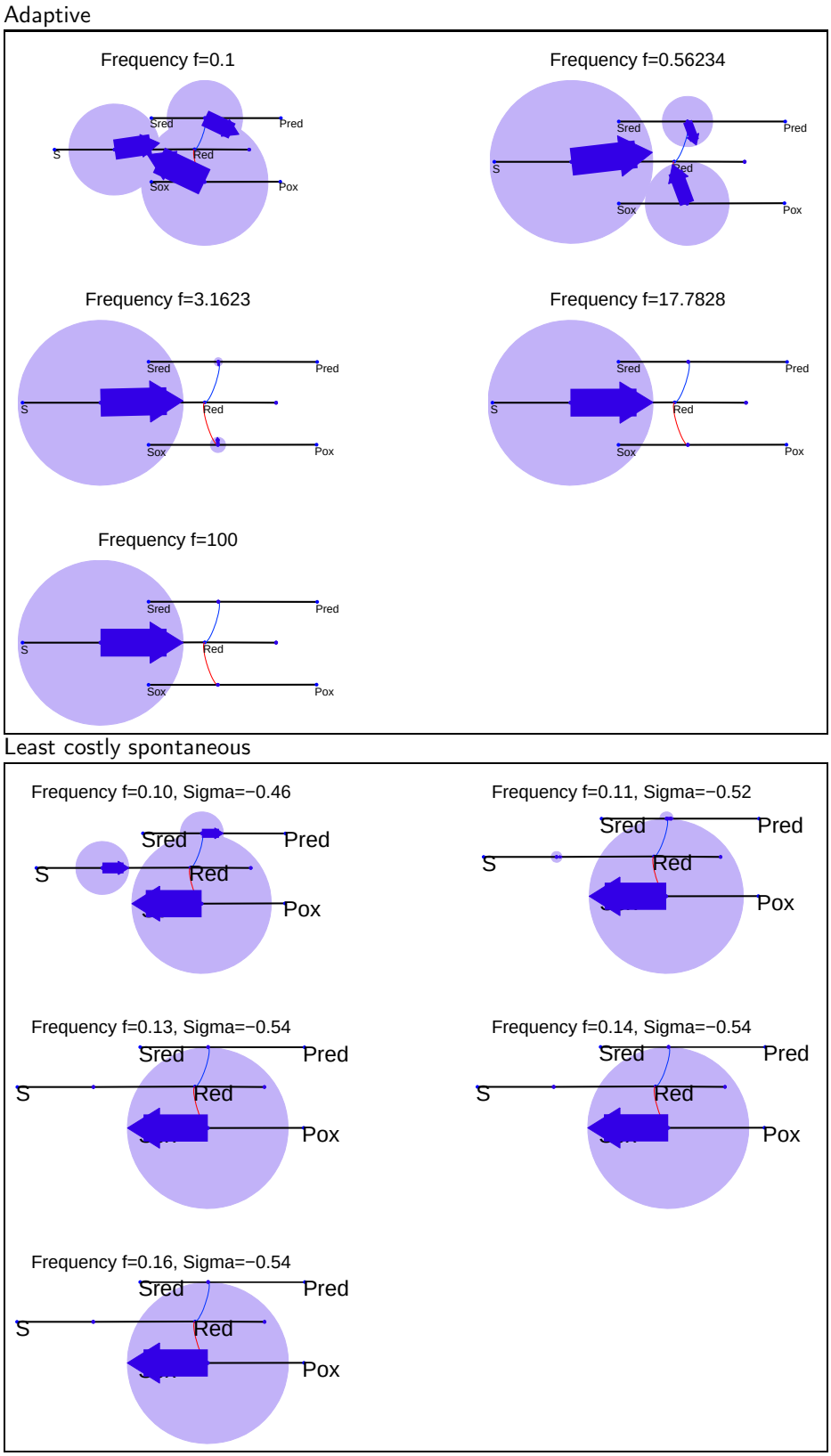


Figure 11: Potential oscillations at various frequencies (local expansion).